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Arg Ala Leu Arg Val His Ser Val Val Ser Val Tyr Met Cys Asn Leu 50 60

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Thr Gly Ala Ile Phe Gln Met Asn Met Tyr Gly Ser Cys Ile Phe Leu 100 105 110

Met Leu Ile Asn Val Asp Arg Tyr Ala Ala Ile Val His Pro Leu Arg 115 120 125

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Tyr Ser Ser Gly Arg Val Phe Trp Thr Leu Ala Arg Pro Asp Ala Thr 210 215 220

Gln Ser Gln Arg Arg Lys Thr Val Arg Leu Leu Leu Ala Asn Leu 225 230 235 240

Tyr Gly Leu Leu Arg Ser Lys Leu Val Ala Ala Ser Val Pro Ala Arg 260 265 270

Asp Arg Val Arg Gly Val Leu Met Val Met Val Leu Leu Ala Gly Ala 275 280 285

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Arg Asn Thr Leu Arg Gly Leu Gly Thr Pro His Arg Ala Arg Thr Ser 305 310 315 320

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His Thr		Gln Th	r Leu	Ala		Val	Val	Tyr	Val		Val	Leu		
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W-1 W-1	Clar Dha	D 7.1	- 7	G	T	0	T	m	Db.	01	m	T		
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- Cys Cys Ile Ser Val Asp Arg Tyr Leu Ala Val Ala His Pro Phe Arg 115 120 125
- Phe His Gln Phe Arg Thr Leu Lys Ala Ala Val Gly Val Ser Val Val 130 135 140
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- Glu Val Ile Glu Asp Glu Asn Gln His Arg Val Cys Phe Glu His Tyr 165 170 175
- Pro Ile Gln Ala Trp Gln Arg Ala Ile Asn Tyr Tyr Arg Phe Leu Val 180 185 190
- Gly Phe Leu Phe Pro Ile Cys Leu Leu Leu Ala Ser Tyr Gln Gly Ile 195 200 205
- Leu Arg Ala Val Arg Arg Ser His Gly Thr Gln Lys Ser Arg Lys Asp 210 215 220
- Gln Ile Gln Arg Leu Val Leu Ser Thr Val Val Ile Phe Leu Ala Cys 225 230 235 240
- Phe Leu Pro Tyr His Val Leu Leu Val Arg Ser Val Trp Glu Ala 245 250 255
- Ser Cys Asp Phe Ala Lys Gly Val Phe Asn Ala Tyr His Phe Ser Leu 260 265 270
- Leu Leu Thr Ser Phe Asn Cys Val Ala Asp Pro Val Leu Tyr Cys Phe 275 280 285
- Val Ser Glu Thr Thr His Arg Asp Leu Ala Arg Leu Arg Gly Ala Cys 290 295 300

Leu Ala Phe Leu Thr Cys Ser Arg Thr Gly Arg Ala Arg Glu Ala Tyr 305 310

Pro Leu Gly Ala Pro Glu Ala Ser Gly Lys Ser Gly Ala Gln Gly Glu 325 330

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Gln Ile Lys Ala Arg Asn Glu Leu Gly Val Tyr Leu Cys Asn Leu Thr

Val Ala Asp Leu Phe Tyr Ile Cys Ser Leu Pro Phe Trp Leu Gln Tyr 70

Val Leu Gln His Asp His Trp Ser His Asp Asp Leu Ser Cys Gln Val 90

Cys Gly Ile Leu Leu Tyr Glu Asn Ile Tyr Ile Ser Val Gly Phe Leu

Cys Cys Ile Ser Ile Asp Arg Tyr Leu Ala Val Ala His Pro Phe Arg

Phe His Gln Phe Arg Thr Leu Lys Ala Ala Met Gly Val Ser Ala Leu

130 135 140

Ile Trp Val Lys Glu Leu Leu Thr Ser Ile Tyr Phe Leu Met His Glu Glu Val Val Glu Asp Ala Asp Arg His Arg Val Cys Phe Glu His Tyr Pro Leu Glu Pro Arg Gln Arg Gly Ile Asn Tyr Tyr Arg Phe Leu Val Gly Phe Leu Phe Pro Ile Cys Leu Leu Ala Ser Tyr Arg Gly Ile Leu Arg Ala Val Arg Arg Ser His Gly Thr Gln Lys Ser Arg Lys Asp Gln Ile Gln Arg Leu Val Leu Ser Thr Val Val Ile Phe Leu Ala Cys Phe Leu Pro Tyr His Val Leu Leu Val Arg Ser Leu Trp Glu Ser Ser Cys Asp Phe Ala Lys Gly Ile Phe Asn Ala Tyr His Phe Ser Leu Leu Leu Thr Ser Phe Asn Cys Val Ala Asp Pro Val Leu Tyr Cys Phe Val Ser Glu Thr Thr His Arg Asp Leu Ala Arg Leu Arg Gly Ala Cys Leu Ala Phe Leu Thr Cys Ala Arg Thr Gly Arg Ala Arg Glu Ala Tyr Pro Leu Gly Ala Pro Glu Ala Ser Gly Lys Ser Glu Asp Pro Glu Val Leu Thr Arg Leu His Pro Ala Phe Gln Thr Pro His Pro Pro Gly Met

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Val Phe Ile Leu Gly Leu Ile Thr Asn Ser Val Ser Leu Phe Val Phe 50 55 60

Cys Phe Arg Met Lys Met Arg Ser Glu Thr Ala Ile Phe Ile Thr Asn 70 75 80

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Ile Ser Gly Thr Ala Phe Leu Thr Asn Ile Tyr Gly Ser Met Leu Phe 115 120 125

Leu Thr Cys Ile Ser Val Asp Arg Phe Leu Ala Ile Val Tyr Pro Phe 130 135 140

Arg Ser Arg Thr Ile Arg Thr Arg Arg Asn Ser Ala Ile Val Cys Ala 145 150 155 160

Gly Val Trp Ile Leu Val Leu Ser Gly Gly Ile Ser Ala Ser Leu Phe 165 170 175

Ser Thr Thr Asn Val Asn Asn Ala Thr Thr Val Cys Phe Glu His Tyr 180 185 190

Pro Leu Glu Pro Arg Gln Arg Gly Ile Asn Tyr Tyr Arg Phe Leu Val 200 195 205 Gly Phe Leu Phe Pro Ile Cys Leu Leu Ala Ser Tyr Arg Gly Ile 210 215 220 Leu Arg Ala Val Arg Arg Ser His Gly Thr Leu Ser Gln Ile Gly Thr 225 230 235 240 Asn Lys Lys Val Leu Lys Met Ile Thr Val His Met Ala Val Phe 245 250 Val Val Cys Phe Val Pro Tyr Asn Ser Val Leu Phe Leu Tyr Ala Leu 260 265 270 Val Arg Ser Gln Ala Ile Thr Asn Cys Phe Leu Glu Arg Phe Ala Lys 275 280 Ile Met Tyr Pro Ile Thr Leu Cys Leu Ala Thr Leu Asn Cys Cys Phe Asp Pro Phe Ile Tyr Tyr Phe Thr Leu Glu Ser Phe Gln Lys Ser Phe 310 Tyr Ile Asn Ala His Ile Arg Met Glu Ser Leu Phe Lys Thr Glu Thr 330 Pro Leu Thr Thr Lys Pro Ser Leu Pro Ala Ile Gln Glu Glu Val Ser Asp Gln Thr Thr Asn Asn Gly Gly Glu Leu Met Leu Glu Ser Thr Phe 360 <210> 11 <211> 370 <212> PRT <213> Homo sapiens <400> 11 Met Gly Asp Arg Arg Phe Ile Asp Phe Gln Phe Gln Asp Ser Asn Ser 5

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Gly Thr Asn Lys Lys Val Leu Lys Met Ile Thr Val His Met Ala

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Ala Leu Val Arg Ser Gln Ala Ile Thr Asn Cys Phe Leu Glu Arg Phe 275 280 285

Ala Lys Ile Met Tyr Pro Ile Thr Leu Cys Leu Ala Thr Leu Asn Cys 290 295 300

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Leu Ala Ile Val His Pro Phe Arg Ser Lys Thr Leu Arg Thr Lys Arg 115 120 125

Asn Ala Arg Ile Val Cys Val Ala Val Trp Ile Thr Val Leu Ala Gly 130 135 140

Ser Thr Pro Ala Ser Phe Phe Gln Ser Thr Asn Arg Gln Asn Asn Thr 145 150 155 160

Glu Gln Arg Thr Cys Phe Glu Asn Phe Pro Glu Ser Thr Trp Lys Thr 165 170 175

Tyr Leu Ser Arg Ile Val Ile Phe Ile Glu Ile Val Gly Phe Phe Ile 180 185 190

Pro Leu Ile Leu Asn Val Thr Cys Ser Thr Met Val Leu Arg Thr Leu 195 200 205

Asn Lys Pro Leu Thr Leu Ser Arg Asn Lys Leu Ser Lys Lys Val 210 215 220

Leu Lys Met Ile Phe Val His Leu Val Ile Phe Cys Phe Cys Phe Val 225 230 235 240

Pro Tyr Asn Ile Thr Leu Ile Leu Tyr Ser Leu Met Arg Thr Gln Thr 245 250 255

Trp Ile Asn Cys Ser Val Val Thr Ala Val Arg Thr Met Tyr Pro Val 260 265 270

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Leu Phe Val Phe Thr Leu Pro Phe Arg Ile Phe Tyr Phe Thr Thr Arg 65 70 75 80

Asn Trp Pro Phe Gly Asp Leu Leu Cys Lys Ile Ser Val Met Leu Phe 85 90 95

Tyr Thr Asn Met Tyr Gly Ser Ile Leu Phe Leu Thr Cys. Ile Ser Val 100 105 110

Asp Arg Phe Leu Ala Ile Val Tyr Pro Phe Lys Ser Lys Thr Leu Arg 115 120 125

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Ile Gly Gly Ser Ala Pro Ala Val Phe Val Gln Ser Thr His Ser Gln 145 150 155 160

Gly Asn Asn Ala Ser Glu Ala Cys Phe Glu Asn Phe Pro Glu Ala Thr 165 170 175

Trp Lys Thr Tyr Leu Ser Arg Ile Val Ile Phe Ile Glu Ile Val Gly 180 185 190

Phe Phe Ile Pro Leu Ile Leu Asn Val Thr Cys Ser Ser Met Val Leu 195 200 205

Lys Thr Leu Thr Lys Pro Val Thr Leu Ser Arg Ser Lys Ile Asn Lys 210 215 220

Thr Lys Val Leu Lys Met Ile Phe Val His Leu Ile Ile Phe Cys Phe 225 230 235 240

Cys Phe Val Pro Tyr Asn Ile Asn Leu Ile Leu Tyr Ser Leu Val Arg 245 250 255

Thr Gln Thr Phe Val Asn Cys Ser Val Val Ala Ala Val Arg Thr Met $260 \\ \hspace{1.5cm} 265 \\ \hspace{1.5cm} 270 \\ \hspace{1.5cm}$

Tyr Pro Ile Thr Leu Cys Ile Ala Val Ser Asn Cys Cys Phe Asp Pro 275 280 285

Ile Val Tyr Tyr Phe Thr Ser Asp Thr Ile Gln Asn Ser Ile Lys Met 290 295 . 300

Lys Asn Trp Ser Val Arg Arg Ser Asp Phe Arg Phe Ser Glu Val His 305 310 315 320

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Leu Phe Ala Ser Phe Tyr Leu Leu Asp Phe Ile Leu Ala Leu Val Gly Asn Thr Leu Ala Leu Trp Leu Phe Ile Arg Asp His Lys Ser Gly Thr Pro Ala Asn Val Phe Leu Met His Leu Ala Val Ala Asp Leu Ser Cys Val Leu Val Leu Pro Thr Arg Leu Val Tyr His Phe Ser Gly Asn His Trp Pro Phe Gly Glu Ile Ala Cys Arg Leu Thr Gly Phe Leu Phe Tyr Leu Asn Met Tyr Ala Ser Ile Tyr Phe Leu Thr Cys Ile Ser Ala Asp Arg Phe Leu Ala Ile Val His Pro Val Lys Ser Leu Lys Leu Arg Arg Pro Leu Tyr Ala His Leu Ala Cys Ala Phe Leu Trp Val Val Ala Val Ala Met Ala Pro Leu Leu Val Ser Pro Gln Thr Val Gln Thr Asn His Thr Val Val Cys Leu Gln Leu Tyr Arg Glu Lys Ala Ser His His Ala Leu Val Ser Leu Ala Val Ala Phe Thr Phe Pro Phe Ile Thr Thr Val Thr Cys Tyr Leu Leu Ile Ile Arg Ser Leu Arg Gln Gly Leu Arg Val Glu Lys Arg Leu Lys Thr Lys Ala Val Arg Met Ile Ala Ile Val Leu Ala Ile Phe Leu Val Cys Phe Val Pro Tyr His Val Asn Arg Ser

Val Tyr Val Leu His Tyr Arg Ser His Gly Ala Ser Cys Ala Thr Gln 260 265 270

Arg Ile Leu Ala Leu Ala Asn Arg Ile Thr Ser Cys Leu Thr Ser Leu 275 280 285

Asn Gly Ala Leu Asp Pro Ile Met Tyr Phe Phe Val Ala Glu Lys Phe 290 295 300

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Ser Glu Leu

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Asn Ala Pro Thr Leu Trp Leu Phe Leu Phe Arg Leu Arg Pro Trp Asp 50 55 60

Ala Thr Ala Thr Tyr Met Phe His Leu Ala Leu Ser Asp Thr Leu Tyr 65 70 75 80

Val Leu Ser Leu Pro Thr Leu Val Tyr Tyr Ala Ala Arg Asn His
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Trp Pro Phe Gly Thr Gly Leu Cys Lys Phe Val Arg Phe Leu Phe Tyr

100 105 110

Trp	Asn	Leu	Tyr	Cys	Ser	Val	Leu	Phe	Leu	Thr	Cys	Ile	Ser	Val	His
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- Pro Arg Phe Ala Ser Leu Leu Cys Leu Gly Val Trp Leu Val Val Ala 145 150 155 160
- Gly Cys Leu Val Pro Asn Leu Phe Phe Val Thr Thr Asn Ala Asn Gly 165 170 175
- Thr Thr Ile Leu Cys His Asp Thr Thr Leu Pro Glu Glu Phe Asp His 180 185 190
- Tyr Val Tyr Phe Ser Ser Ala Val Met Val Leu Leu Phe Gly Leu Pro 195 200 205
- Phe Leu Ile Thr Leu Val Cys Tyr Gly Leu Met Ala Arg Arg Leu Tyr 210 215 220
- Arg Pro Leu Pro Gly Ala Gly Gln Ser Ser Ser Arg Leu Arg Ser Leu 225 230 235 240
- Arg Thr Ile Ala Val Val Leu Thr Val Phe Ala Val Cys Phe Val Pro 245 250 255
- Phe His Ile Thr Arg Thr Ile Tyr Tyr Gln Ala Arg Leu Leu Gln Ala 260 265 270
- Asp Cys His Val Leu Asn Ile Val Asn Val Val Tyr Lys Val Thr Arg 275 280 285 ·
- Pro Leu Ala Ser Ala Asn Ser Cys Leu Asp Pro Val Leu Tyr Leu Phe 290 295 300
- Thr Gly Asp Lys Tyr Arg Asn Gln Leu Gln Gln Leu Cys Arg Gly Ser 305 310 315 320
- Lys Pro Lys Pro Arg Thr Ala Ala Ser Ser Leu Ala Leu Val Thr Leu 325 330 335

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Ala Ile Gln Cys Ile Tyr Ala Leu Val Cys Leu Val Gly Leu Val Gly 50 55 60

Asn Ala Leu Val Ile Phe Val Ile Leu Arg Tyr Ala Lys Met Lys Thr 65 70 75 80

Ala Thr Asn Ile Tyr Leu Leu Asn Leu Ala Val Ala Asp Glu Leu Phe 85 90 95

Met Leu Ser Val Pro Phe Val Ala Ser Ser Ala Ala Leu Arg His Trp 100 105 110

Pro Phe Gly Ser Val Leu Cys Arg Ala Val Leu Ser Val Asp Gly Leu 115 120 125

Asn Met Phe Thr Ser Val Phe Cys Leu Thr Val Leu Ser Val Asp Arg 130 135 140

Tyr Val Ala Val Val His Pro Leu Arg Ala Ala Thr Tyr Arg Arg Pro 145 150 155 160

Ser Val Ala Lys Leu Ile Asn Leu Gly Val Trp Leu Ala Ser Leu Leu Val Thr Leu Pro Ile Ala Ile Phe Ala Asp Thr Arg Pro Ala Arg Gly Gly Gln Ala Val Ala Cys Asn Leu Gln Trp Pro His Pro Ala Trp Ser Ala Val Phe Val Val Tyr Thr Phe Leu Leu Gly Phe Leu Leu Pro Val Leu Ala Ile Gly Leu Cys Tyr Leu Leu Ile Val Gly Lys Met Arg Ala Val Ala Leu Arg Ala Gly Trp Gln Gln Arg Arg Arg Ser Glu Lys Lys Ile Thr Arg Leu Val Leu Met Val Val Val Phe Val Leu Cys Trp Met Pro Phe Tyr Val Val Gln Leu Leu Asn Leu Val Val Thr Ser Leu Asp Ala Thr Val Asn His Val Ser Leu Ile Leu Ser Tyr Ala Asn Ser Cys Ala Asn Pro Ile Leu Tyr Gly Phe Leu Ser Asp Asn Phe Arg Arg Ser Phe Gln Arg Val Leu Cys Leu Arg Cys Cys Leu Leu Glu Gly Ala Gly Gly Ala Glu Glu Pro Leu Asp Tyr Tyr Ala Thr Ala Leu Lys Ser Lys Gly Gly Ala Gly Cys Met Cys Pro Pro Leu Pro Cys Gln Gln Glu Ala Leu Gln Pro Glu Pro Gly Arg Lys Arg Ile Pro Leu Thr Arg

Thr Thr Thr Phe

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<223> n is a, c, g, or t

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<223> This codon may be replaced by TTR
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aargtntgga thccnacntc nacntggctn caracn
                                                                       36
<210>
       84
<211>
       36
<212>
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<213>
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<221> misc_feature
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      (10)..(12)
<223>
      This codon may be replaced by AGN
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      (13)..(15)
<223> This codon may be replaced by TTR
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      (22)..(24)
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      (27)..(27)
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<223> n is a, c, g, or t
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aargtntggt cnctngayat htcngcnccn carcay
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       This codon may be replaced by TTR
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      (21)..(21)
<223> n is a, c, g, or t
<220>
<221>
      misc feature
<222>
      (24)..(24)
<223>
      n is a, c, g, or t
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      misc feature
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      (25)..(27)
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       This codon may be replaced by AGY
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<223> This codon may be replaced by TTR
<400> 85
                                                                       45
gengaygtne theaygenae neentengar aargtntgge theth
<210>
       86
<211> 45
<212> DNA
<213> Artificial
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<220>
<221> misc_feature
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<223> n is a, c, g, or t
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<222> (13)..(15)
<223> This codon may be replaced by AGY
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<222> (27)..(27)
<223> n is a, c, g, or t
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<221> misc feature
<222> (31)..(33)
<223> This codon may be replaced by TTR
<220>
<221> misc feature
<222>
      (36)..(36)
<223> n is a, c, g, or t
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<221> misc_feature
<222>
      (37)..(39)
<223> This codon may be replaced by AGY
<220>
<221> misc_feature
<222> (45)..(45)
<223> n is a, c, g, or t
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aargtngtng aytcnaayca yaargtntgg ctngtntcnc aracn
                                                                      45
<210>
      87
<211>
      36
<212> DNA
<213> Artificial
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      (31)..(33)
<223>
     This codon may be replaced by TTR
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      (36)..(36)
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<400> 87
aaycaygaya ayacnaaraa rgtntggath ctngcn
                                                                      36
<210> 88
<211> 39
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      (16)..(18)
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<400> 86

<220>

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<220>
<221>
      misc_feature
<222>
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<223>
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<400> 88
aarctnttrt ggathctngc ngayaaytty acnaaycgn
                                                                      39
<210> 89
<211>
      45
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      DNA
<213>
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<221> misc_feature
<222> (19)..(21)
<223> This codon may be replaced by TTR
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<223>
      This codon may be replaced by TTR
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      misc_feature
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      (34)..(36)
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      This codon may be replaced by TTR
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<221>
      misc_feature
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      (37)..(39)
<223> This codon may be replaced by TTR
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<223> n is a, c, g, or t
<400> 89
athaaytcnc encaygaret naaraaretn tggetnetne encen
                                                                      45
<210>
       90
<211>
       36
<212>
       DNA
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<223> n is a, c, g, or t
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<221> misc_feature
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      (13)..(15)
<223> This codon may be replaced by TTR
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<221> misc_feature
<222> (21)..(21)
<223> n is a, c, g, or t
<220>
<221> misc feature
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      (22)..(24)
<223> This codon may be replaced by TTR
<220>
<221> misc feature
<222> (27)..(27)
<223> n is a, c, g, or t
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<221>
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      (30)..(30)
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      n is a, c, g, or t
<220>
<221> misc_feature
<222> (36)..(36)
<223> n is a, c, g, or t
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<400> 90
ttyccncaya arctntgggt nctnccngtn aaracn
                                                                       36
<210> 91
<211> 36
<212> DNA
<213> Artificial
<220>
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<223> This codon may be replaced by TTR
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<222> (12)...(12)
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      (18)..(18)
<223> n is a, c, g, or t
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<221> misc_feature
<222> (19)..(21)
<223> This codon may be replaced by AGY
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<222> (33)..(33)
<223> n is a, c, g, or t
<220>
<221> misc_feature
<222> (36)..(36)
<223> n is a, c, g, or t
<400> 91
aarctntgga cnathcente naaygaytay cencen
                                                                       36
<210> 92
<211> 36
<212>
      DNA
<213>
      Artificial
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<223> oligonucleotide
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<222> (13)..(15)
<223> This codon may be replaced by TTR
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<222> (21)..(21)
<223> n is a, c, g, or t
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<221>
      misc_feature
<222> (24)..(24)
<223> n is a, c, g, or t
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      (27)..(27)
<223> n is a, c, g, or t
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<221> misc_feature
<222> (30)..(30)
<223> n is a, c, g, or t
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      (33)..(33)
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<220>
<221> misc_feature
<222> (36)..(36)
<223> n is a, c, g, or t
<400> 92
aarctntggg arctntaycc nacngtnccn gcnggn
                                                                     36
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      93
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      36
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<223> This codon may be replaced by TTR
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<223> n is a, c, g, or t
<220>
<221> misc feature
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      (21)..(21)
<223> n is a, c, g, or t
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      (22)..(24)
<223> This codon may be replaced by AGY
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      (30)..(30)
<223> n is a, c, g, or t
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<221>
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<223>
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<400> 93
aarctntgga thccncayac ntcncarccn ttyctn
                                                                      36
<210>
       94
<211>
       36
<212>
      DNA
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      Artificial
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<223>
      This codon may be replaced by TTR
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      misc feature
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      (18)..(18)
<223>
      n is a, c, g, or t
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      misc feature
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      (21)..(21)
<223>
      n is a, c, g, or t
<220>
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      misc feature
<222> (24)..(24)
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<223> n is a, c, g, or t
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<221> misc_feature
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       (25)..(27)
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<222> (30)...(30)
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<400> 94
aarctntggg ayathacngc nccnctnccn aarccn
                                                                       36
<210> 95
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<223> n is a, c, g, or t
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<222> (10)..(12)
<223> This codon may be replaced by TTR
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<222> (24)..(24)
<223> n is a, c, g, or t
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<222> (27)..(27)
<223> n is a, c, g, or t
<220>
<221>
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<222>
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<223> n is a, c, g, or t
<400> 95
aaygcnaarc tntggcarat hccngcnath ccncay
                                                                       36
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      (12)..(12)
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      n is a, c, g, or t
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<223> n is a, c, g, or t
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      (22)..(24)
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      This codon may be replaced by AGR
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      (36)..(36)
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aarctntggg tnccncaraa ycgnccngar ctngtn
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      97
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      36
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       (4)..(6)
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       (13)..(15)
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       This codon may be replaced by TTR
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      (21)..(21)
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      n is a, c, g, or t
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      (27)..(27)
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      n is a, c, g, or t
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      n is a, c, g, or t
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      (36)..(36)
      n is a, c, g, or t
<223>
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aarctntggg arctntaycc nacngtnccn gcnggn
                                                                       36
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       98
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       36
<212>
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<221> misc_feature
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<222> (3)..(3)
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<223> This codon may be replaced by AGY
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<223> n is a, c, g, or t
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      (12)..(12)
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<223> n is a, c, g, or t
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<221> misc_feature
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      (28)..(30)
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      This codon may be replaced by TTR
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<221> misc_feature
<222> (33)..(33)
<223> n is a, c, g, or t
<220>
<221> misc feature
<222>
      (36)..(36)
<223> n is a, c, g, or t
<400> 98
acntenaene encayegngt ntggearetn cengtn
                                                                      36
<210> 99
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      45
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<213>
      Artificial
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<223> n is a, c, g, or t
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<223> n is a, c, g, or t
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      misc feature
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      (9)..(9)
<223> n is a, c, g, or t
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      (13)..(15)
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      This codon may be replaced by AGR
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      (18)..(18)
<223> n is a, c, g, or t
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      (25)..(27)
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      This codon may be replaced by TTR
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<221> misc_feature
<222> (30)..(30)
<223> n is a, c, g, or t
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      (31)..(33)
<223>
      This codon may be replaced by TTR
<220>
<221> misc_feature
<222> (39)..(39)
<223> n is a, c, g, or t
<400> 99
                                                                      45
acnaencene ayegngtntg gaayetneen etngargene arear
<210> 100
<211> 45
<212>
      DNA
<213>
      Artificial
<220>
<223> oligonucleotide
<400> 100
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<210> <211> <212> <213>	101 45 DNA Artificial	
<220> <223>	oligonucleotide	
<400> agtagg	101 gtgt ctggtgcgaa ggtttggttt ttgagtaatt ggtct	45
	102 36 DNA Artificial	
<220> <223>	oligonucleotide	
<400> gctatg	102 aata gtcataagat ttggatgttg ccgcat	36
<210> <211> <212> <213>	103 36 DNA Artificial	
<220> <223>	oligonucleotide	
<400> ggtctg	103 aaga tttggagttt geegeegeat eatggg	36
<210> <211> <212> <213>	104 36 DNA Artificial	
<220> <223>	oligonucleotide	
<400> aaggtt	104 tggt agatggcgcc tacgactgcg ttttcg	36
<210><211><211><212><213>	105 45 DNA Artificial	
<220>		

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<223> oligonucleotide
<220>
       misc_feature
<221>
<222>
      (3)..(3)
<223> n is a, c, g, or t
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       (9)..(9)
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      n is a, c, g, or t
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      (15)..(15)
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      This codon may be replaced by AGR
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<222> (24)..(24)
<223> n is a, c, g, or t
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      (28)..(30)
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      This codon may be replaced by AGY
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<222> (33)..(33)
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      (36)..(36)
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      misc feature
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      (40)..(42)
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      This codon may be replaced by AGR
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<221>
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<223> This codon may be replaced by AGY
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acneayggnt tyggneayeg ngtntggten gtneenetne gnten
<210> 106
<211> 45
<212> DNA
<213> Artificial
<220>
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      (31)..(33)
<223> This codon may be replaced by TTR
<220>
<221> misc_feature
<222> (34)..(36)
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45

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<223> This codon may be replaced by AGY
<220>
<221> misc_feature
<222> (43)..(45)
<223> This codon may be replaced by AGY
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tenegngtht enggngenaa rgthtggtty ethtenaayt ggten
                                                                       45
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<211> 36
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<222> (10)...(12) <223> This codon may be replaced by AGY
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      (28)..(30)
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<221> misc_feature
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<223> n is a, c, g, or t
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gcnatgaayt cncayaarat htggatgctn ccncay
                                                                       36
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<211> 36
<212> DNA
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<223> oligonucleotide
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<222> (3)..(3)
<223> n is a, c, g, or t
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      misc_feature
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      (4)..(6)
<223> This codon may be replaced by TTR
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      (16)..(18)
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      (19)..(21)
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      This codon may be replaced by TTR
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      (24)..(24)
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      n is a, c, g, or t
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<222>
      (36)..(36)
<223>
      n is a, c, g, or t
<400> 108
                                                                      36
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      (34)..(36)
      This codon may be replaced by AGY
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      Homo sapiens
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                5
                                    10
Ile Glu Asn Phe Lys Arg Glu Phe Phe Pro Ile Val Tyr Leu Ile Ile
            20
Phe Phe Trp Gly Val Leu Gly Asn Gly Leu Ser Ile Tyr Val Phe Leu
        35
                            40
Gln Pro Tyr Lys Lys Ser Thr Ser Val Asn Val Phe Met Leu Asn Leu
    50
Ala Ile Ser Asp Leu Leu Phe Ile Ser Thr Leu Pro Phe Arg Ala Asp
Tyr Tyr Leu Arg Gly Ser Asn Trp Ile Phe Gly Asp Leu Ala Cys Arg
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36

Ile Met Ser Tyr Ser Leu Tyr Val Asn Met Tyr Ser Ser Ile Tyr Phe 100 1.05 110 Leu Thr Val Leu Ser Val Val Arg Phe Leu Ala Met Val His Pro Phe 115 120 Arg Leu Leu His Val Thr Ser Ile Arg Ser Ala Trp Ile Leu Cys Gly 130 135 140 Ile Ile Trp Ile Leu Ile Met Ala Ser Ser Ile Met Leu Leu Asp Ser Gly Ser Glu Gln Asn Gly Ser Val Thr Ser Cys Leu Glu Leu Asn Leu 170 Tyr Lys Ile Ala Lys Leu Gln Thr Met Asn Tyr Ile Ala Leu Val Val 185 Gly Cys Leu Leu Pro Phe Phe Thr Leu Ser Ile Cys Tyr Leu Leu Ile 200 Ile Arg Val Leu Leu Lys Val Glu Val Pro Glu Ser Gly Leu Arg Val 210 Ser His Arg Lys Ala Leu Thr Thr Ile Ile Ile Thr Leu Ile Ile Phe 230 235 Phe Leu Cys Phe Leu Pro Tyr His Thr Leu Arg Thr Val His Leu Thr 250 Thr Trp Lys Val Gly Leu Cys Lys Asp Arg Leu His Lys Ala Leu Val Ile Thr Leu Ala Leu Ala Ala Ala Asn Ala Cys Phe Asn Pro Leu Leu Tyr Tyr Phe Ala Gly Glu Asn Phe Lys Asp Arg Leu Lys Ser Ala Leu Arg Lys Gly His Pro Gln Lys Ala Lys Thr Lys Cys Val Phe Pro Val 310 315

Ser Val Trp Leu Arg Lys Glu Thr Arg Val

325 330

<210> 111 <211> 337

<212> PRT

<213> Homo sapiens

<400> 111

Met Asn Glu Pro Leu Asp Tyr Leu Ala Asn Ala Ser Asp Phe Pro Asp 1 5 10 15

Tyr Ala Ala Ala Phe Gly Asn Cys Thr Asp Glu Asn Ile Pro Leu Lys 20 25 30

Met His Tyr Leu Pro Val Ile Tyr Gly Ile Ile Phe Leu Val Gly Phe 35 40 45

Pro Gly Asn Ala Val Val Ile Ser Thr Tyr Ile Phe Lys Met Arg Pro 50 55 60

Trp Lys Ser Ser Thr Ile Ile Met Leu Asn Leu Ala Cys Thr Asp Leu 65 70 75 80

Leu Tyr Leu Thr Ser Leu Pro Phe Leu Ile His Tyr Tyr Ala Ser Gly 85 90 95

Glu Asn Trp Ile Phe Gly Asp Phe Met Cys Lys Phe Ile Arg Phe Ser

Phe His Phe Asn Leu Tyr Ser Ser Ile Leu Phe Leu Thr Cys Phe Ser 115 120 125

Ile Phe Arg Tyr Cys Val Ile Ile His Pro Met Ser Cys Phe Ser Ile 130 135 140

His Lys Thr Arg Cys Ala Val Val Ala Cys Ala Val Val Trp Ile Ile 145 150 155 160

Ser Leu Val Ala Val Ile Pro Met Thr Phe Leu Ile Thr Ser Thr Asn 165 170 175

Arg Thr Asn Arg Ser Ala Cys Leu Asp Leu Thr Ser Ser Asp Glu Leu 180 185 190 Asn Thr Ile Lys Trp Tyr Asn Leu Ile Leu Thr Ala Thr Thr Phe Cys 195 200 205

Leu Pro Leu Val Ile Val Thr Leu Cys Tyr Thr Thr Ile Ile His Thr 210 215 220

Leu Thr His Gly Leu Gln Thr Asp Ser Cys Leu Lys Gln Lys Ala Arg 225 230 235 240

Arg Leu Thr Ile Leu Leu Leu Leu Ala Phe Tyr Val Cys Phe Leu Pro 245 250 255

Phe His Ile Leu Arg Val Ile Arg Ile Glu Ser Arg Leu Leu Ser Ile 260 265 270

Ser Cys Ser Ile Glu Asn Gln Ile His Glu Ala Tyr Ile Val Ser Arg 275 280 285

Pro Leu Ala Ala Leu Asn Thr Phe Gly Asn Leu Leu Tyr Val Val 290 295 300

Val Ser Asp Asn Phe Gln Gln Ala Val Cys Ser Thr Val Arg Cys Lys 305 310 315 320

Val Ser Gly Asn Leu Glu Gln Ala Lys Lys Ile Ser Tyr Ser Asn Asn 325 330 335

Pro

<210> 112

<211> 339

<212> PRT

<213> Homo sapiens

<400> 112

Ser Thr Ser Thr Ala Glu Ile Tyr Cys Asn Val Thr Asn Val Lys Phe

Gln Tyr Ser Leu Tyr Ala Thr Thr Tyr Ile Leu Ile Phe Ile Pro Gly

35 40 45

- Leu Leu Ala Asn Ser Ala Ala Leu Trp Val Leu Cys Arg Phe Ile Ser 50 55 60
- Lys Lys Asn Lys Ala Ile Ile Phe Met Ile Asn Leu Ser Val Ala Asp 65 . 70 75 80
- Leu Ala His Val Leu Ser Leu Pro Leu Arg Ile Tyr Tyr Ile Ser 85 90 95
- His His Trp Pro Phe Gln Arg Ala Leu Cys Leu Leu Cys Phe Tyr Leu 100 105 110
- Lys Tyr Leu Asn Met Tyr Ala Ser Ile Cys Phe Leu Thr Cys Ile Ser 115 120 125
- Leu Gln Arg Cys Phe Phe Leu Leu Lys Pro Phe Arg Ala Arg Asp Trp 130 135 140
- Lys Arg Arg Tyr Asp Val Gly Ile Ser Ala Ala Ile Trp Ile Val Val 145 150 155 160
- Gly Thr Ala Cys Leu Pro Phe Pro Ile Leu Arg Ser Thr Asp Leu Asn 165 170 175
- Asn Asn Lys Ser Cys Phe Ala Asp Leu Gly Tyr Lys Gln Met Asn Ala 180 185 190
- Val Ala Leu Val Gly Met Ile Thr Val Ala Glu Leu Ala Gly Phe Val 195 200 205
- Ile Pro Val Ile Ile Ile Ala Trp Cys Thr Trp Lys Thr Thr Ile Ser 210 215 220
- Leu Arg Gln Pro Pro Met Ala Phe Gln Gly Ile Ser Glu Arg Gln Lys 225 230 235 240
- Ala Leu Arg Met Val Phe Met Cys Ala Ala Val Phe Phe Ile Cys Phe 245 250 255
- Thr Pro Tyr His Ile Asn Phe Ile Phe Tyr Thr Met Val Lys Glu Thr 260 265 270

Ile Ile Ser Ser Cys Pro Val Val Arg Ile Ala Leu Tyr Phe His Pro $275 \hspace{1.5cm} 280 \hspace{1.5cm} 285$

Phe Cys Leu Cys Leu Ala Ser Leu Cys Cys Leu Leu Asp Pro Ile Leu 290 295 300

Tyr Tyr Phe Met Ala Ser Glu Phe Arg Asp Gln Leu Ser Arg His Gly 305 310 315 320

Ser Ser Val Thr Arg Ser Arg Leu Met Ser Lys Glu Ser Gly Ser Ser 325 330 335

Met Ile Gly